REMARKS

Claims 1, 2 and 4-11 are pending. Claims 1 and 2 are allowed.

Applicants have submitted an Information Disclosure Statement for the Examiner's consideration in view of the Request for Continued Examination submitted herewith.

Claims 4-11 are rejected under the written description requirement of 35 U.S.C. § 112 first paragraph. For reasons set forth below rejection of the claims should be withdrawn and all pending claims be allowed to issue.

The Claims Comply With The Written Description Requirement

Claims 4-11 are rejected under 35 U.S.C. §112, first paragraph.

According to the Examiner:

> [A]mended claim 4 recites the limitation of an isolated nucleic acid sequence having 90% homology with SEQ ID NO:1 and "the protein encoded by the nucleic acid molecule comprises a caspase recruitment domain and a RNA helicase domain . . . ." However, there is no support in the specification for the claimed nucleic acid(s) because the passages cited by the Applicants (page 52, lines 6-8, and page 57, lines 21-25) are directed to Mda-5 polynucleotide and polypeptide only. The specification teaches that Mda-5 is encoded by cDNA as disclosed in SEQ ID NO:1, not nucleic acid having 90% homology of SEQ ID NO:1. Therefore, such recitation constitutes new matter.

Thus according to the Examiner, passages cited to support amended claim 4 (and claims dependent thereon) are directed to Mda-5 protein rather than nucleic acid and that the specification allegedly does not provide for nucleic acids with 90% homology to SEQ ID NO:1. Because the Examiner contends that specification fails to support the claimed nucleic acids in amended claim 4, the rejection of claims 4-11 is maintained.

In response, Applicants assert that the subject matter encompassed by amended claim is 4 fully supported in the specification in compliance with 35 U.S.C. §112, first paragraph, and therefore the rejection should be withdrawn. Applicants assert that the Examiner has not fully considered the response to a similar rejection filed August 10, 2005 in which amendments to claim 4 fully overcome the presently re-applied rejection. Applicants respectfully disagree that new matter has been introduced due to amendments filed in the prior response.

The Examiner has alleged that the passages cited by the Applicants at page 52, lines 6-8,

> "Ectopic expression of mda-5 reduces the colony-forming efficiency of HO-1 melanoma cells by ~70%, which suggests a growth inhibitory or a pro-apoptotic role of mda-5."

and page 57, lines 21-25,

> "Electronic sequence analysis of the MDA-5 protein using motif and profile scans of proteins presently in the protein database identified two conserved domains, a caspase recruitment domain (CARD) and an RNA helicase domain."

do not provide support for nucleic acids with 90% homology to SEQ ID NO:1 since the cited passages refer to Mda-5 protein. The Applicants' reason for citing the specification at pages 52 and 57 was to support an additional limitation introduced into claim 4 i.e., to a nucleic acid encoding a protein comprising a caspase recruitment domain and a RNA helicase domain. This limitation was introduced to more clearly set forth the nature of the homology relationship and to require that the encompassed molecules encode proteins which, like MDA-5 protein having SEQ ID NO:2, comprise a caspase recruitment domain and an RNA helicase domain. The passages were not, as implied as by the Examiner, cited in support of a nucleic acid having 90% homology to SEQ ID NO:1.

Support for nucleic acids having 90% homology to SEQ ID NO:1 may be found at page 27, line 23 through page 28, line 6,

> "Two DNA or polypeptide sequences are "substantially homologous" when at least about 80% (preferably at least about 90%, and most preferably at least about 95%) of the nucleotides or amino acids match over a defined length of the molecule. As used herein, "substantially homologous" also refers to sequences showing identity to the specified DNA or polypeptide sequence. DNA sequences that are substantially homologous can be identified in a Southern hybridization, experiment under, for example, stringent conditions, as defined for that particular system. Defining appropriate hybridization conditions is within the skill of the art. See, e.g., Sambrook et al., supra; DNA Cloning, vols I & II, supra; Nucleic Acid Hybridization, supra."

and has been previously cited e.g. in the response filed March 29, 2004 (at page 5). These amendments do not result in the introduction of new matter as contended by the Examiner. The Examiner has merely reiterated a rejection that is fully addressed in prior responses. Applicants assert that the person skilled in the art would easily understand or be able to practice the invention of claim 4 and its dependent claims. A skilled practitioner will easily know what entity is specified by a molecule that: (i) possesses 90% homology to SEQ ID NO.1; (ii) possess two structural limitations, a caspase recruitment domain and a RNA helicase domain; and (iii) possess a functional limitation to reduce colony forming ability of HO-1 melanoma cells.

The combination of homology, structural and functional limitations specified in claim 4 will provide all necessary guidance to a skilled practitioner. Applicants therefore believe that claim 4 in its present form is fully enabled by the specification, so that the rejection of claim 4 and its dependent claims should be removed.

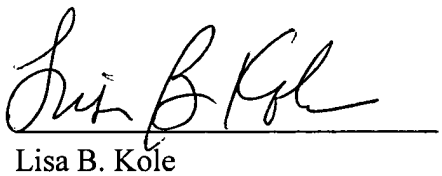
CONCLUSION

Based on the foregoing remarks, Applicants submit that the present application is in condition for allowance. A Notice of Allowance is therefore respectfully requested.

Applicants do not believe that any additional fee is required in connection with the submission of this document. However, should any fee be required, the Commissioner is hereby authorized to charge any fees to Deposit Account 02-4377. A copy of this sheet is enclosed.

Respectfully submitted,

BAKER BOTTS L.L.P.



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